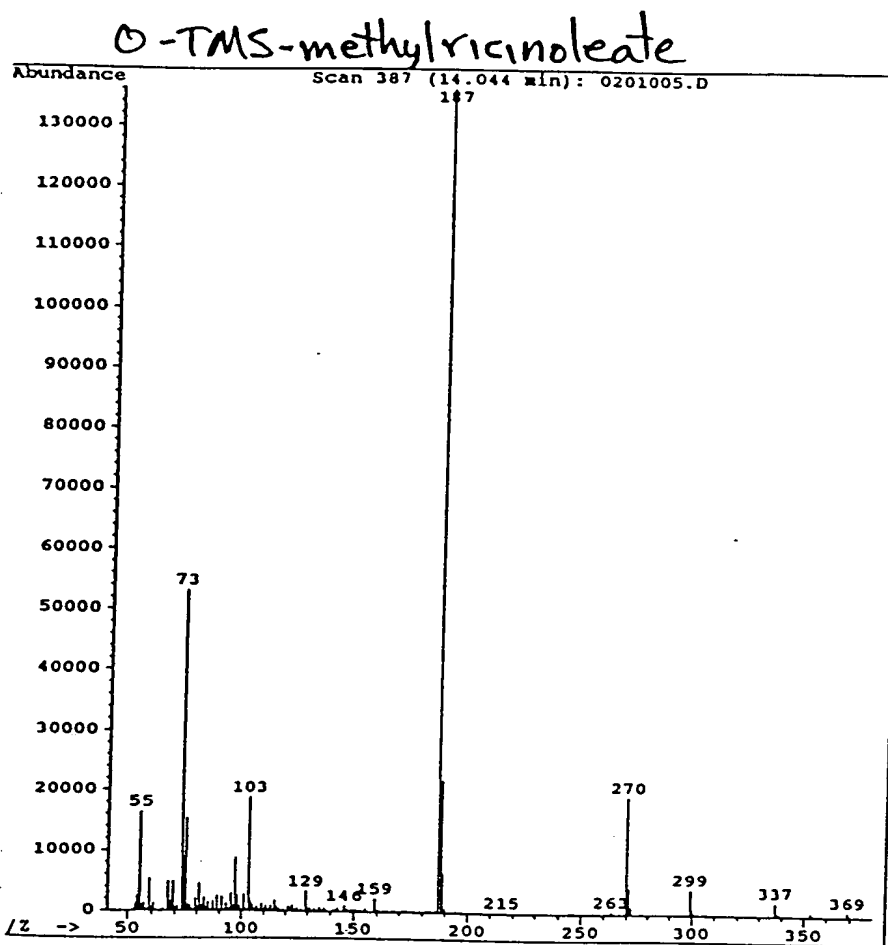
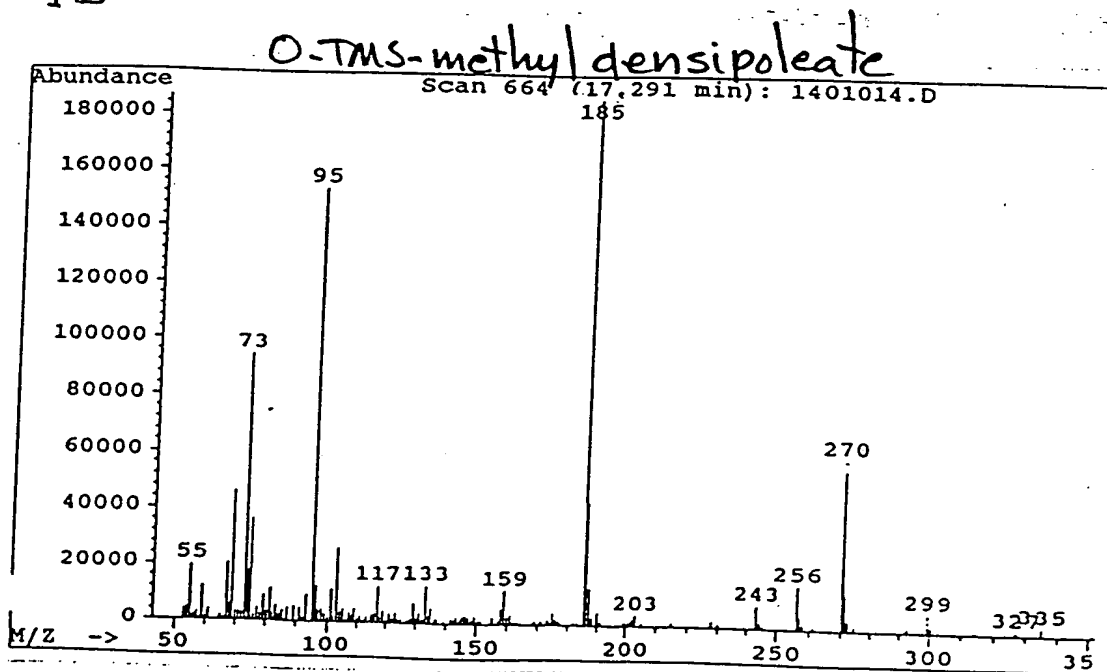


Figure

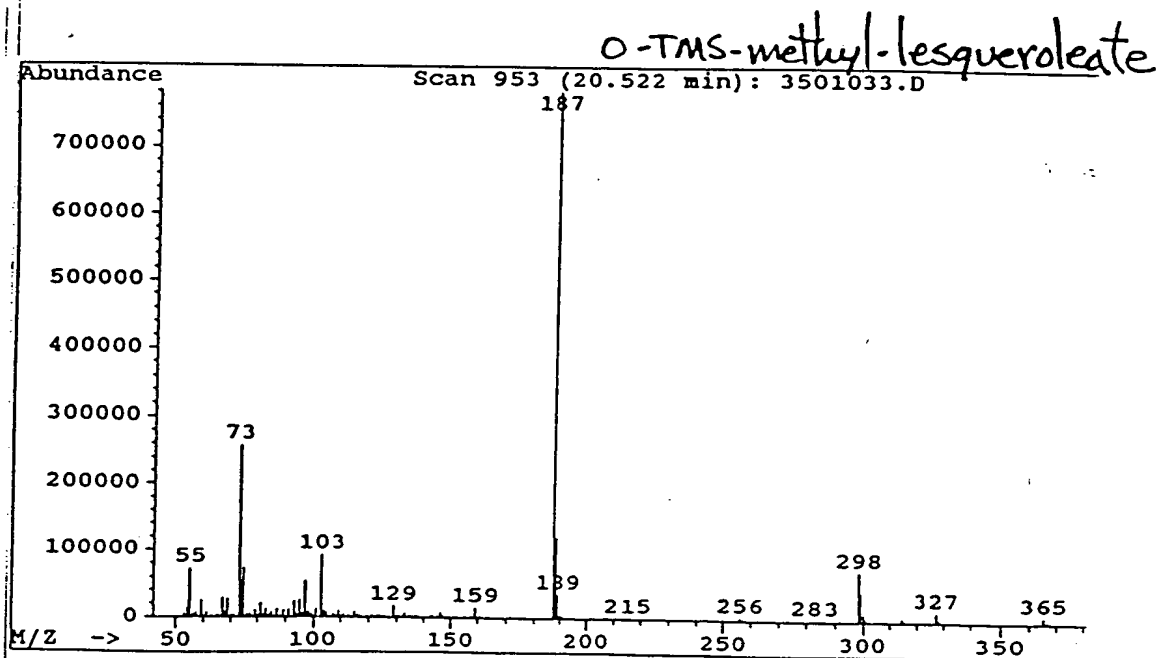
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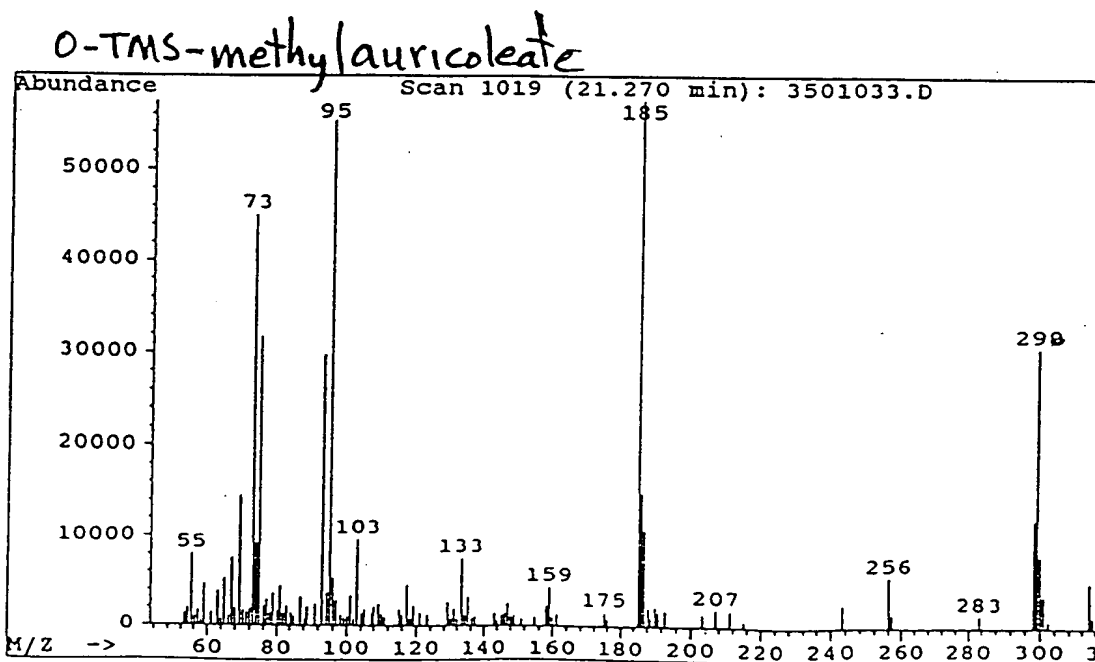
1B



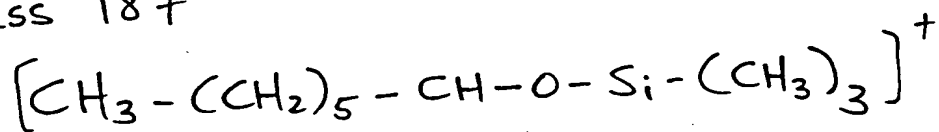
1C



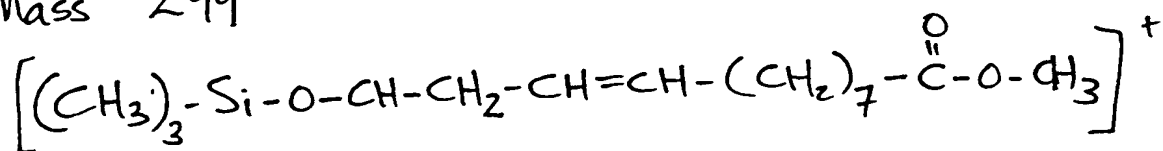
1D



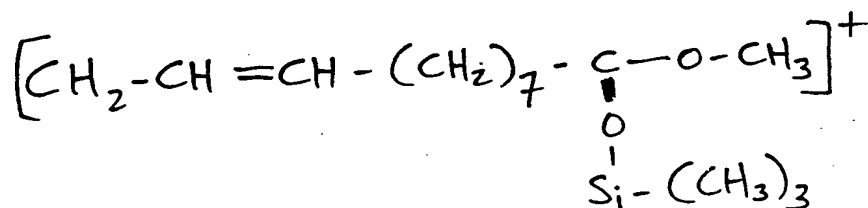
Ion #1: Mass 187



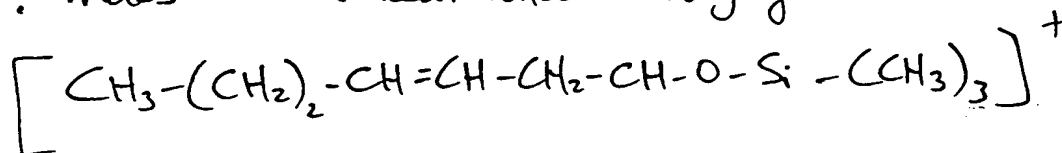
Ion #2: Mass 299



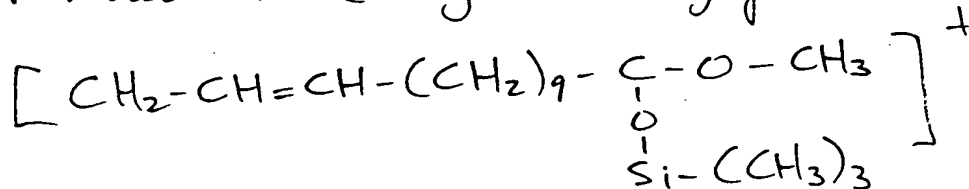
Ion #3: Mass 270 (characteristic rearrangement ion)



Ion #4: Mass 185 (desaturated analog of Ion #1)



Ion #5: Mass 298 (elongated analog of Ion #3)



Ion #6: Mass 327 (elongated analog of Ion #2)

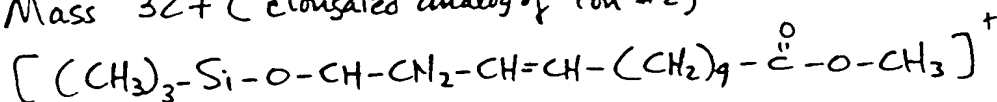


Figure 2.

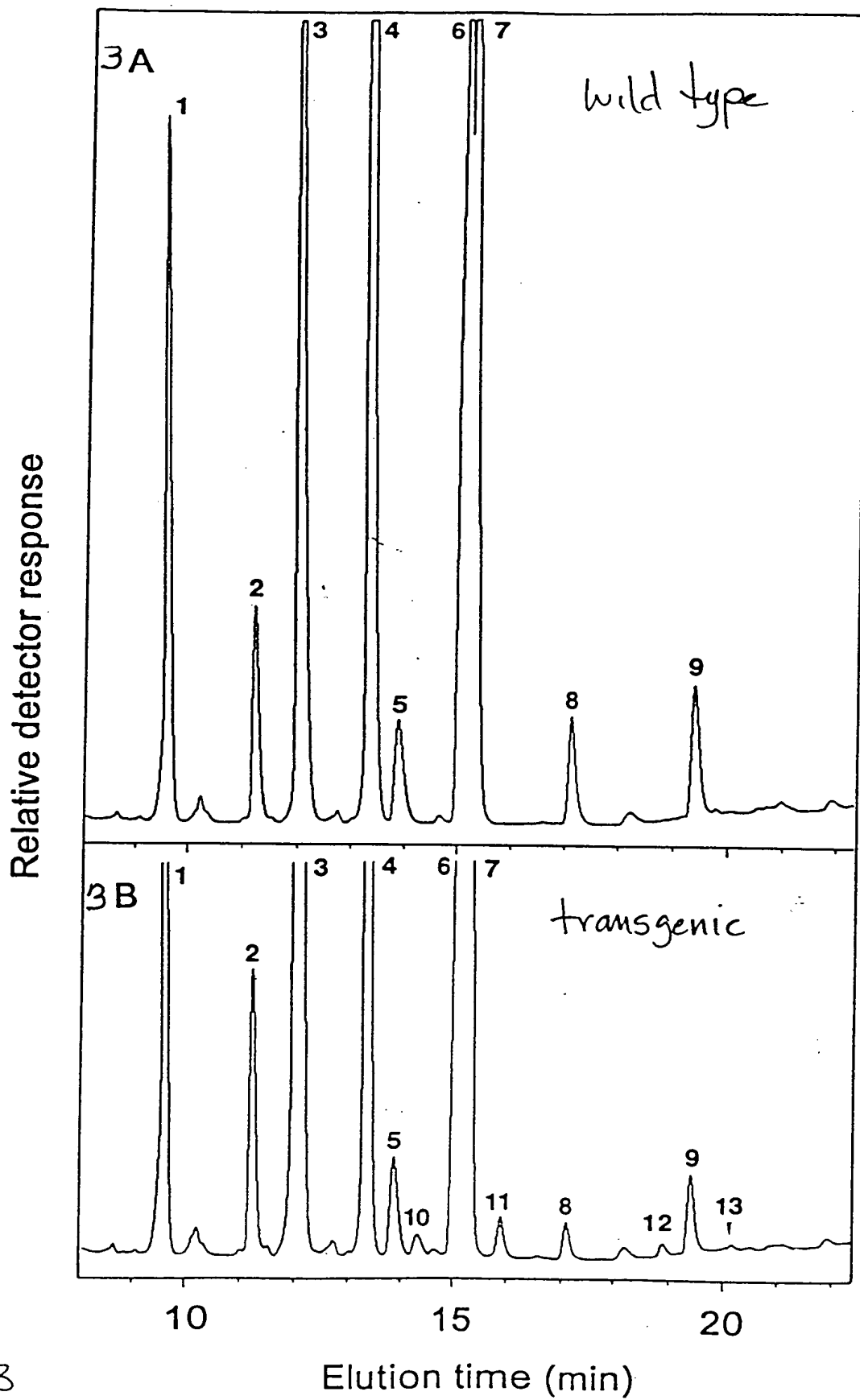
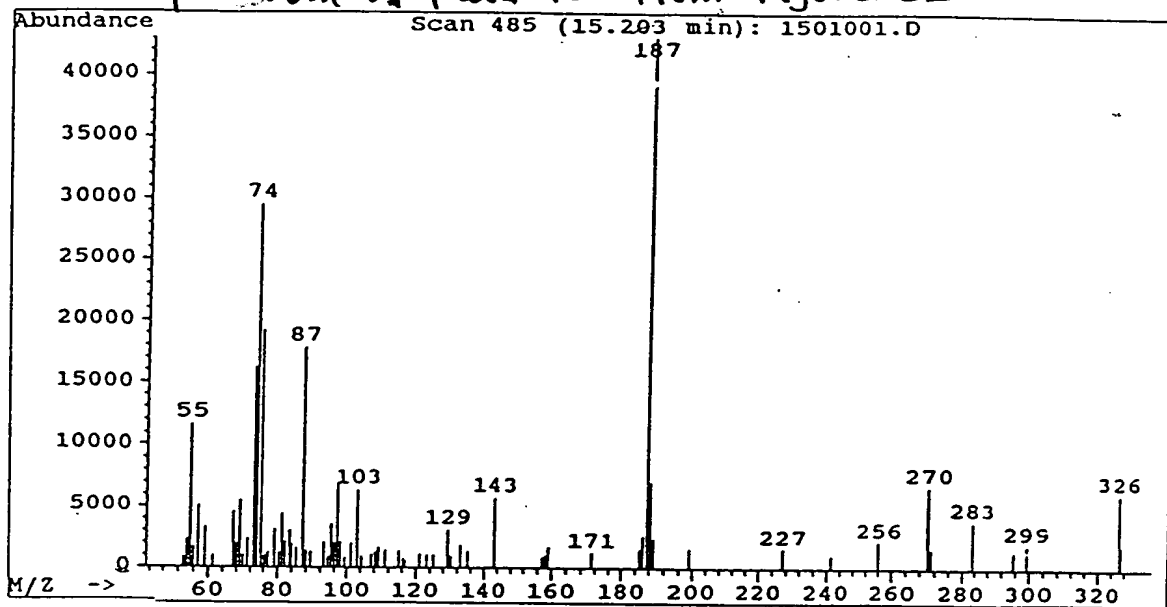


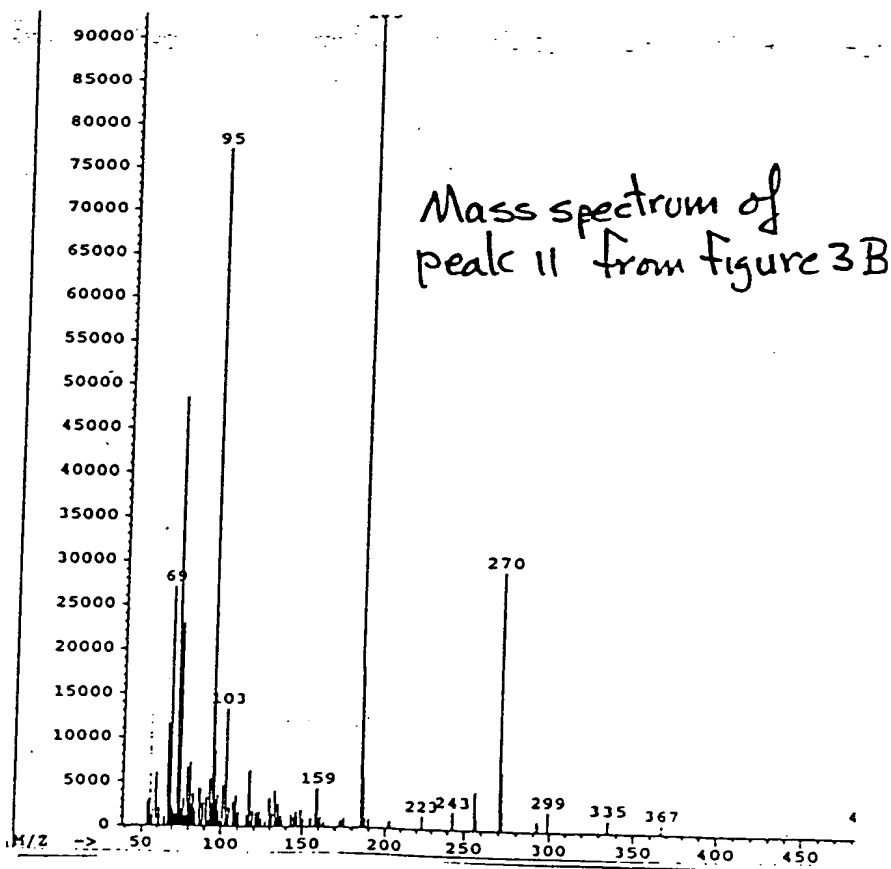
Figure 3

Figure
4A.

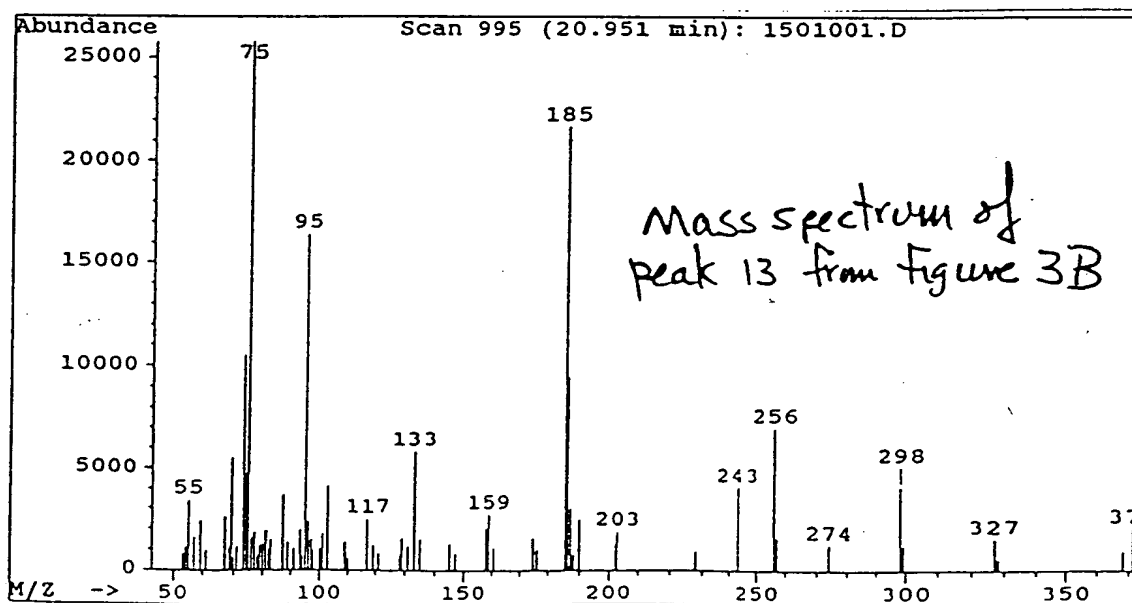
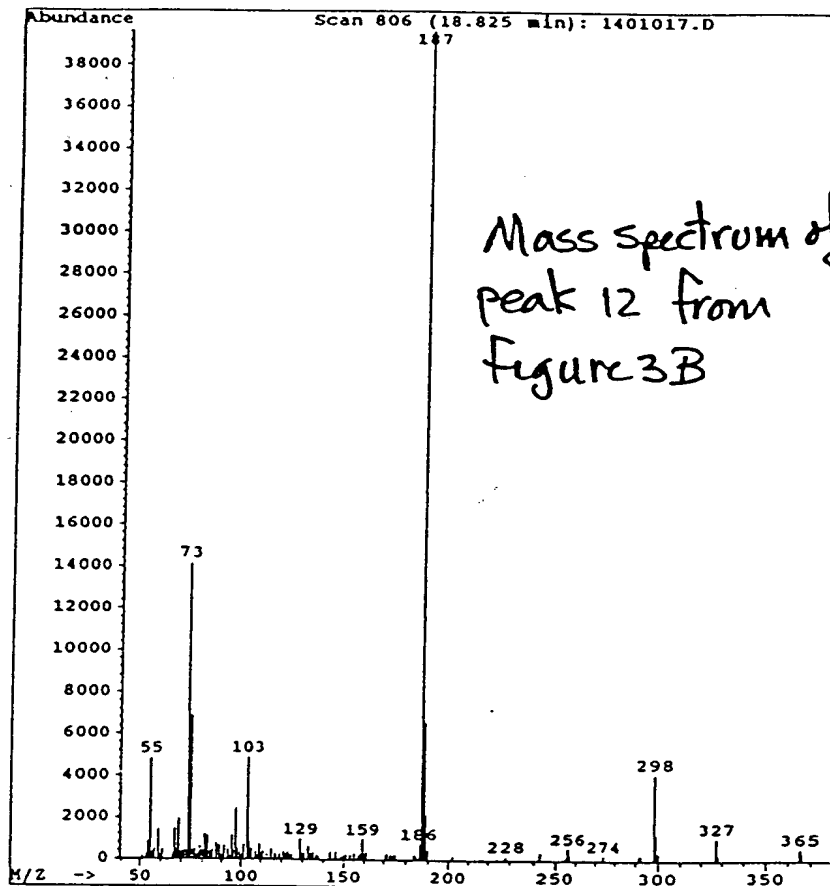
Mass Spectrum of peak 10 from Figure 3B



4B



4C



10	20	30	40	50	60
TATTGGCACC	GGCGGCACCA	TTCCAACAAT	GGATCCCTAG	AAAAAGATGA	AGTCTTTGTC
70	80	90	100	110	120
CCACCTAAGA	AAGCTGCAGT	CANATGGTAT	GTCAAATACC	TCAACAACCC	TCTTGGACGC
130	140	150	160	170	180
ATTCTGGTGT	TAACAGTTCA	GTTTATCCTC	GGGTGGCCTT	TGTATCTAGC	CTTTAATGTA
190	200	210	220	230	240
TCAGGTAGAC	CTTATGATGG	TTTCGCTTCA	CATTTCTTCC	CTCATGCACC	TATCTTTAAG
250	260	270	280	290	300
GACCGTGAAC	GTCTCCAGAT	ATACATCTCA	GATGCTGGTA	TTCTAGCTGT	CTGTTATGGT
310	320	330	340	350	360
CTTTACCGTT	ACGCTGCTTC	ACAAGGATTG	ACTGCTATGA	TCTGCGTCTA	CGGAGTACCG
370	380	390	400	410	420
CTTTTGATAG	TGAACTTTTT	CCTTGTCTTG	GTCACCTTCT	TGCAGCACAC	TCATCCTTCA
430	440	450	460	470	480
TTACCTCACT	ATGATTCAAC	CGAGTGGGAA	TGGATTAGAG	GAGCTTTGGT	TACGGTAGAC
490	500	510	520	530	540
AGAGACTATG	GAATCTTGAA	CAAGGTGTTT	CACAACATAA	CAGACACCCA	CGTAGCACAC
550					

CAC

Figure 5 Nucleotide sequence of pLesq2

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Figure 6 Nucleotide sequence of pLesq3

09885188-052101

Probe
pLesq3

S L

Probe
pLesq2

S L

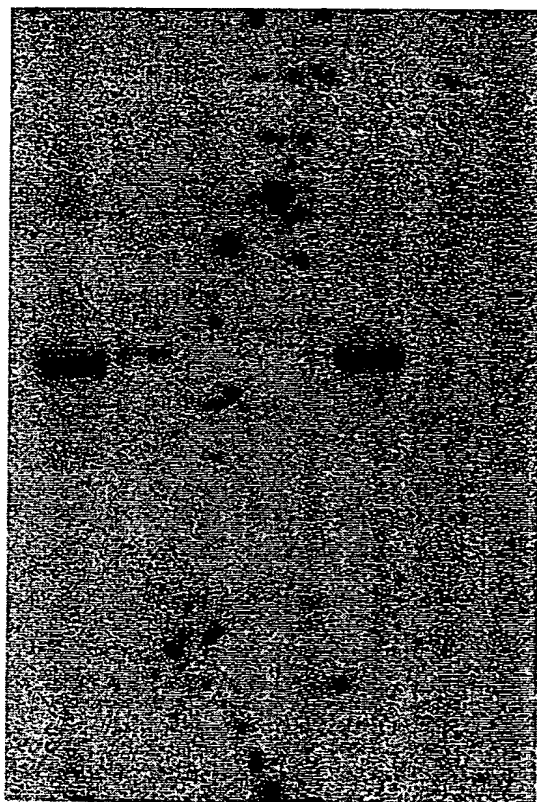


Figure 7

AT	GAA	GCT	TTA	TAA	GAA	GTT	AGT	TTT	CTC	TGG	TGA	CAG	AGA	AAT	TNT	47
GTC	AAT	TGG	TAG	TGA	CAG	TTG	AAG	CAA	CAG	GAA	CAA	CAA	GGA	TGG	TTG	95
GTG	NTG	ATG	CTG	ATG	TGG	TGA	TGT	GTT	ATT	CAT	CAA	ATA	CTA	AAT	ACT	143
ACA	TTA	CTT	GTT	GCT	GCC	TAC	TTC	TCC	TAT	TTC	CTC	CGC	CAC	CCA	TTT	191
TGG	ACC	CAC	GAN	CCT	TCC	ATT	TAA	ACC	CTC	TCT	CGT	GCT	ATT	CAC	CAG	239
AAG	AGA	AGC	CAA	GAG	AGA	GAG	AGA	GAG	AAT	GTT	CTG	AGG	ATC	ATT	GTC	287
TTC	TTC	ATC	GTT	ATT	AAC	GTA	AGT	TTT	TTT	TGA	CCA	CTC	ATA	TCT	AAA	335
ATC	TAG	TAC	ATG	CAA	TAG	ATT	AAT	GAC	TGT	TCC	TTC	TTT	TGA	TAT	TTT	383
CAG	CTT	CTT	GAA	TTC	AAG	Met	Gly	Ala	Gly	Gly	Arg	Ile	Met	Val	Thr	10
						ATG	GGT	GCT	GGT	GGA	AGA	ATA	ATG	GTT	ACC	431
Pro	Ser	Ser	Lys	Lys	Ser	Glu	Thr	Glu	Ala	Leu	Lys	Arg	Gly	Pro	Cys	26
CCC	TCT	TCC	AAG	AAA	TCA	GAA	ACT	GAA	GCC	CTA	AAA	CGT	GGA	CCA	TGT	479
Glu	Lys	Pro	Pro	Phe	Thr	Val	Lys	Asp	Leu	Lys	Lys	Ala	Ile	Pro	Gln	42
GAG	AAA	CCA	CCA	TTC	ACT	GTT	AAA	GAT	CTG	AAG	AAA	GCA	ATC	CCA	CAG	527
His	Cys	Phe	Lys	Arg	Ser	Ile	Pro	Arg	Ser	Phe	Ser	Tyr	Leu	Leu	Thr	58
CAT	TGT	TTC	AAG	CGC	TCT	ATC	CCT	CGT	TCT	TTC	TCC	TAC	CTT	CTC	ACA	575
Asp	Ile	Thr	Leu	Val	Ser	Cys	Phe	Tyr	Tyr	Val	Ala	Thr	Asn	Tyr	Phe	74
GAT	ATC	ACT	TTA	GTT	TCT	TGC	TTC	TAC	TAC	GTT	GCC	ACA	AAT	TAC	TTC	623
Ser	Leu	Leu	Pro	Gln	Pro	Leu	Ser	Thr	Tyr	Leu	Ala	Trp	Pro	Leu	Tyr	90
TCT	CTT	CTT	CCT	CAG	CCT	CTC	TCT	ACT	TAC	CTA	GCT	TGG	CCT	CTC	TAT	671
Trp	Val	Cys	Gln	Gly	Cys	Val	Leu	Thr	Gly	Ile	Trp	Val	Ile	Gly	His	106
TGG	GTA	TGT	CAA	GGC	TGT	GTC	TTA	ACC	GGT	ATC	TGG	GTC	ATT	GGC	CAT	719
Glu	Cys	Gly	His	His	Ala	Phe	Ser	Asp	Tyr	Gln	Trp	Val	Asp	Asp	Thr	122
GAA	TGT	GGT	CAC	CAT	GCA	TTC	AGT	GAC	TAT	CAA	TGG	GTA	GAT	GAC	ACT	767
Val	Gly	Phe	Ile	Phe	His	Ser	Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	138
GTT	GGT	TTT	ATC	TTC	CAT	TCC	TTC	CTT	CTC	GTC	CCT	TAC	TTC	TCC	TGG	815
Lys	Tyr	Ser	His	Arg	Arg	His	His	Ser	Asn	Asn	Gly	Ser	Leu	Glu	Lys	154
AAA	TAC	AGT	CAT	CGT	CGT	CAC	CAT	TCC	AAC	AAT	GGA	TCT	CTC	GAG	AAA	863
Asp	Glu	Val	Phe	Val	Pro	Pro	Lys	Lys	Ala	Ala	Val	Lys	Trp	Tyr	Val	170
GAT	GAA	GTC	TTT	GTC	CCA	CCG	AAG	AAA	GCT	GCA	GTC	AAA	TGG	TAT	GTT	911
Lys	Tyr	Leu	Asn	Asn	Pro	Leu	Gly	Arg	Ile	Leu	Val	Leu	Thr	Val	Gln	186
AAA	TAC	CTC	AAC	AAC	CCT	CTT	GGA	CGC	ATT	CTG	GTG	TTA	ACA	GTT	CAG	959

Figure 8A

Phe	Ile	Leu	Gly	Trp	Pro	Leu	Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	202
TTT	ATC	CTC	GGG	TGG	CCT	TTG	TAT	CTA	GCC	TTT	AAT	GTA	TCA	GGT	AGA	1007
Pro	Tyr	Asp	Gly	Phe	Ala	Ser	His	Phe	Phe	Pro	His	Ala	Pro	Ile	Phe	218
CCT	TAT	GAT	GGT	TTC	GCT	TCA	CAT	TTC	TTC	CCT	CAT	GCA	CCT	ATC	TTT	1055
Lys	Asp	Arg	Glu	Arg	Leu	Gln	Ile	Tyr	Ile	Ser	Asp	Ala	Gly	Ile	Leu	234
AAA	GAC	CGA	GAA	CGC	CTC	CAG	ATA	TAC	ATC	TCA	GAT	GCT	GGT	ATT	CTA	1103
Ala	Val	Cys	Tyr	Gly	Leu	Tyr	Arg	Tyr	Ala	Ala	Ser	Gln	Gly	Leu	Thr	250
GCT	GTC	TGT	TAT	GGT	CTT	TAC	CGT	TAC	GCT	GCT	TCA	CAA	GGA	TTG	ACT	1151
Ala	Met	Ile	Cys	Val	Tyr	Gly	Val	Pro	Leu	Leu	Ile	Val	Asn	Phe	Phe	266
GCT	ATG	ATC	TGC	GTC	TAT	GGA	GTA	CCG	CTT	TTG	ATA	GTG	AAC	TTT	TTC	1199
Leu	Val	Leu	Val	Thr	Phe	Leu	Gln	His	Thr	His	Pro	Ser	Leu	Pro	His	282
CTT	GTC	TTG	GTA	ACT	TTC	TTG	CAG	CAC	ACT	CAT	CCT	TCG	TTA	CCT	CAT	1247
Tyr	Asp	Ser	Thr	Glu	Trp	Glu	Trp	Ile	Arg	Gly	Ala	Leu	Val	Thr	Val	298
TAT	GAT	TCA	ACC	GAG	TGG	GAA	TGG	ATT	AGA	GGA	GCT	TTG	GTT	ACG	GTA	1295
Asp	Arg	Asp	Tyr	Gly	Ile	Leu	Asn	Lys	Val	Phe	His	Asn	Ile	Thr	Asp	314
GAC	AGA	GAC	TAT	GGA	ATA	TTG	AAC	AAG	GTG	TTC	CAT	AAC	ATA	ACA	GAC	1343
Thr	His	Val	Ala	His	His	Leu	Phe	Ala	Thr	Ile	Pro	His	Tyr	Asn	Ala	330
ACA	CAT	GTG	GCT	CAT	CAT	CTC	TTT	GCA	ACT	ATA	CCG	CAT	TAT	AAC	GCA	1391
Met	Glu	Ala	Thr	Glu	Ala	Ile	Lys	Pro	Ile	Leu	Gly	Asp	Tyr	Tyr	His	346
ATG	GAA	GCT	ACA	GAG	GCG	ATA	AAG	CCA	ATA	CTT	GGT	GAT	TAC	TAC	CAC	1439
Phe	Asp	Gly	Thr	Pro	Trp	Tyr	Val	Ala	Met	Tyr	Arg	Glu	Ala	Lys	Glu	362
TTC	GAT	GGA	ACA	CCG	TGG	TAT	GTG	GCC	ATG	TAT	AGG	GAA	GCA	AAG	GAG	1487
Cys	Leu	Tyr	Val	Glu	Pro	Asp	Thr	Glu	Arg	Gly	Lys	Lys	Gly	Val	Tyr	378
TGT	CTC	TAT	GTA	GAA	CCG	GAT	ACG	GAA	CGT	GGG	AAG	AAA	GGT	GTC	TAC	1535
Tyr	Tyr	Asn	Asn	Lys	Leu											384
TAT	TAC	AAC	AAT	AAG	TTA	TGA	GGC	TGA	TAG	GGC	GAG	AGA	AGT	GCA	ATT	1583
ATC	AAT	CTT	CAT	TTC	CAT	GTT	TTA	GGT	GTC	TTG	TTT	AAG	AAG	CTA	TGC	1631
TTT	GTT	TCA	ATA	ATC	TCA	GAG	TCC	ATN	TAG	TTG	TGT	TCT	GGT	GCA	TTT	1679
TGC	CTA	GTT	ATG	TGG	TGT	CGG	AAG	TTA	GTG	TTC	AAA	CTG	CTT	CCT	GCT	1727
GTG	CTG	CCC	AGT	GAA	GAA	CAA	GTT	TAC	GTG	TTT	AAA	ATA	CTC	GGA	ACG	1775
AAT	TGA	CCA	CAA	NAT	ATC	CAA	AAC	CGG	CTA	TCC	GAA	TTC	CAT	ATC	CGA	1823
AAA	CCG	GAT	ATC	CAA	ATT	TCC	AGA	GTA	CTT	AG						1855

Figure 8B

	10	20	30	40	50	
LFFAH12.AMI	1	MGAGGRIM-- --VTPSSKKS	--ETEALKRG	PCEKPPFTVK	DLKKAIPQHC	
FAH12.AMI	1	MGGGGRMSTV	ITSNNSEKKG	--GSSHLKRA	PHTKPPFTLG	DLKRAIPPHC 50
ATFAD2.AMI	1	MGAGGRMP-- --VPTSSKKS	--ETDITKRV	PCEKPPFSVG	DLKKAIPPHC	50
BNFAD2.AMI	1	MGAGGRMQ-- --VSPPSKKS	--ETDNIKRV	PCETPPFTVG	ELKKAIPPHC	50
GMFAD2-1.AMI	1	MGLA-KETTM	GGRGRVAKVE	VQGKKPLSRV	PNTKPPFTVG	QLKKAIPPHC 50
GMFAD2-2.AMI	1	MGAGGR----	TDVPPANRKS	--EVDPLKRV	PFEKPQFSLS	QIKKAIPPHC 50
ZMFAD2.AMI	1	MGAGGRMTEK	EREKQEQLAR	ATGGAAMQRS	PVEKPPFTLG	QIKKAIPPHC 50
RCFAD2.AMI	1	-----	-----	-----	-----	50
		60	70	80	90	100
LFFAH12.AMI	51	FKRSIPRSFS	YLLTDITIVS	CFYYVATNYF	SLLPQPLSTY	LAWPLYWVCQ 100
FAH12.AMI	51	FERSFVRSFS	YVAYDVCLSF	LFYSIATNFF	PYISSPLS-Y	VAWLVIWLFQ 100
ATFAD2.AMI	51	FKRSIPRSFS	YLISDIIIAS	CFYYVATNYF	SLLPQPLS-Y	LAWPLYWACQ 100
BNFAD2.AMI	51	FKRSIPRSFS	HLIWDIIIAS	CFYYVATTYF	PLLPNPLS-Y	FAWPLYWACQ 100
GMFAD2-1.AMI	51	FQSRLLTSFS	YVVYDLSEAF	IFY-IATTYF	HLLPQPFS-L	IAWPIYWVLQ 100
GMFAD2-2.AMI	51	FQSRVLSFS	YVVYDLTIAF	CLYYVATHYF	HLLPGPLS-F	RGMAIYWAVQ 100
ZMFAD2.AMI	51	FERSVLKSFS	YVVDLVIIAA	ALLYFALAI	PALPSPLR-Y	AAWPLYWIAQ 100
RCFAD2.AMI	51	-----	-----	-----	-----	100
		110	120	130	140	150
LFFAH12.AMI	101	GCVLTGIWVI	GHECGHHAFS	DYQWVDDTVG	FIFHSFLLVP	YFSWKYSHRR 150
FAH12.AMI	101	GCILTGLWVI	GHECGHHAFS	EYQLADDIVG	LIVHSALLVP	YFSWKYSHRR 150
ATFAD2.AMI	101	GCVLTGIWVI	AHECGHHAFS	DYQWLDDTVG	LIFHSFLLVP	YFSWKYSHRR 150
BNFAD2.AMI	101	GCVLTGVWVI	AHECGHAAFS	DYQWLDDTVG	LIFHSFLLVP	YFSWKYSHRR 150
GMFAD2-1.AMI	101	GCLLTGVWVI	AHECGHHAFS	KYQWVDDVVG	LTLHSTLLVP	YFSWKISHRR 150
GMFAD2-2.AMI	101	GCILTGVWVI	AHECGHHAFS	DYQLLDDIVG	LILHSALLVP	YFSWKYSHRR 150
ZMFAD2.AMI	101	G-----	-----AFS	DYSLDDDVVG	LVLHSSLMVP	YFSWKYSHRR 150
RCFAD2.AMI	101	-----WVM	AHDCGHHAFS	DYQLLDDVVG	LILHSCLLVP	YFSWKHSHRR 150
		160	170	180	190	200
LFFAH12.AMI	151	HHSNIGSLEK	DEVFVPPKKA	AVKWYVKYL-	NNPLGRILVL	TVQFILGWPL 200
FAH12.AMI	151	HHSNIGSLER	DEVFVPKSKS	KISWYSKYS-	NNPPGRVLT	AATLLLGWPL 200
ATFAD2.AMI	151	HHSNIGSLER	DEVFVPKQKS	AIKWYGKYL-	NNPLGRIMML	TVQFVLGWPL 200
BNFAD2.AMI	151	HHSNIGSLER	DEVFVPR-RS	QTSSGTAST-	STTFGRVTML	TVQFTLGWPL 200
GMFAD2-1.AMI	151	HHSNIGSLDR	DEVFVPKPKS	KVAFWSKYL-	NNPLGRAVSL	LVTLTIGWPM 200
GMFAD2-2.AMI	151	HHSNIGSLER	DEVFVPKQKS	CIKWYSKYL-	NNPPGRVLT	AVTLTLGWPL 200
ZMFAD2.AMI	151	HHSNIGSLER	DEVFVPKKKE	ALPWYTPYVY	NNPVGRVVHI	VVQLTLGWPL 200
RCFAD2.AMI	151	HHSNIGSLER	DEVFVPKKKS	SIRWYSKYL-	NNPPGRIMTI	AVTSLSGWPL 200
		210	220	230	240	250
LFFAH12.AMI	201	YLAFNVSGRP	YDG-FASHFF	PHAPIFKDRE	RLQIYISDAG	ILAVCYGLYR 250
FAH12.AMI	201	YLAFNVSGRP	YDR-FACHYD	PYGPIFSERE	RLQIYIADLG	IFATTFFVLYQ 250
ATFAD2.AMI	201	YLAFNVSGRP	YDG-FACHFF	PNAPIYNDRE	RLQIYLSDAG	ILAVCFGLYR 250
BNFAD2.AMI	201	YLAFNVSGRP	YDGGFACHFH	PNAPIYNDRE	RLQIYISDAG	ILAVCYGLLP 250
GMFAD2-1.AMI	201	YLAFNVSGRP	YDS-FASHYH	PYAPIYSNRE	RLLIYVSDVA	LFSVTYSLYR 250
GMFAD2-2.AMI	201	YLALNVSGRP	YDR-FACHYD	PYGPIYSDRE	RLQIYISDAG	VLAUVYGLFR 250
ZMFAD2.AMI	201	YLATNASGRP	YPR-FACHFD	PYGPIYNDRE	RAQIFVSDAG	VVAVAFGLYK 250
RCFAD2.AMI	201	YLAFNVSGRP	YDR-FACHYD	PYGPIYNDRE	RIEIFISDAG	VLAUTFGLYQ 250
		260	270	280	290	300
LFFAH12.AMI	251	YAASQGLTAM	ICVYGVPLLI	VNFFLVLTFT	LQHTHPSLPH	YDSTEWEWIR 300
FAH12.AMI	251	ATMAKGLAWV	MRIYGVPLLI	VNCFVLMITY	LQHTHPAIPR	YGSSEWDWLR 300
ATFAD2.AMI	251	YAAAQGMASM	ICLYGVPLLI	VNAFLVLITY	LQHTHPSLPH	YDSSEWDWLR 300
BNFAD2.AMI	251	YAAVQGVASM	VCFLRVPLLI	VNGFLVLITY	LQHTHPSLPH	YDSSEWDWLR 300
GMFAD2-1.AMI	251	VATLKGLVWL	LCVYGVPLLI	VNGFLVTITY	LQHTHFALPH	YDSSEWDWLK 300
GMFAD2-2.AMI	251	LAMAKGLAWV	VCVYGVPLLV	VNGFLVLITY	LQHTHPALPH	YTSSEWDWLR 300
ZMFAD2.AMI	251	LAAAFGVWVW	VRVYAVPLLI	VNAWLVLITY	LQHTHPSLPH	YDSSEWDWLR 300

Figure 9A

RCFAD2.AMI	251	LATAKGLAWV	VCVYGVPLLV	VNSFLVLITF	LQHTHPALPH	YDSSEWDWLR	300
		310	320	330	340	350	
LFFAH12.AMI	301	GALVIVDRDY	GILNKVFHNI	TDTHVAHHLF	ATIPHYNAME	ATEAIKPILG	350
FAH12.AMI	301	GAMVIVDRDY	GVLNKVFHNI	ADTHVAHHLF	ATVPHYHAME	ATKAIKPIMG	350
AD2.AMI	301	GALATVDRDY	GILNKVFHNI	TDTHVAHHLF	STMPHYNAME	ATKAIKPILG	350
BNFAD2.AMI	301	GALATVDRDY	GILNQGFHNI	TDTHEAHHLF	STMPHYHAME	ATKAIKPILG	350
GMFAD2-1.AMI	301	GALATMDRDY	GILNKVFHHI	TDTHVAHHLF	STMPHYHAME	ATNAIKPILG	350
GMFAD2-2.AMI	301	GALATVDRDY	GILNKVFHNI	TDTHVAHHLF	STMPHYHAME	ATKAIKPILG	350
ZMFAD2.AMI	301	GALATMDRDY	GILNRVFHNI	TDTHVAHHLF	STMPHYHAME	ATKAIRPILG	350
RCFAD2.AMI	301	GALATVDRDY	GILNKVFHNI	TDTQVAHHLF	-TMP-----	-----	350
		360	370	380	390	400	
LFFAH12.AMI	351	DYYHFDGTPW	YVAMYREAKE	CLYVEPDTER	GKKGVYYNN	K-L.....	400
FAH12.AMI	351	EYYRYDGTFF	YKALWREAKE	CLFVEPDEGA	PTQGVFWYRN	KY-.....	400
ATFAD2.AMI	351	DYYQFDGTPW	YVAMYREAKE	CIYVEPDREG	DKKGVWYNN	K-L.....	400
BNFAD2.AMI	351	EYYQFDGTPV	VKAMWREAKE	CIYVEPDROG	EKKGVFWYNN	KL*.....	400
GMFAD2-1.AMI	351	EYYQFDDTPF	YKALWREARE	CLYVEPDDEGT	SEKGVWYRN	KY-.....	400
GMFAD2-2.AMI	351	EYYRFDETPF	VKAMWREARE	CIYVEPDQST	ESKGVFWYNN	KL-.....	400
ZMFAD2.AMI	351	DYYHFDPTPV	AKATWREAGE	CIYVEPE---	DRKGVFWYNK	KF*.....	400
RCFAD2.AMI	351	-----	-----	-----	-----	-----	400
		410	420	430	440	450	
LFFAH12.AMI	401	450
FAH12.AMI	401	450
ATFAD2.AMI	401	450
BNFAD2.AMI	401	450
GMFAD2-1.AMI	401	450
GMFAD2-2.AMI	401	450
ZMFAD2.AMI	401	450

Figure 9B

098518-062101

Molecular weight markers



E H X

3.6 -

1.8 -

1.5 -

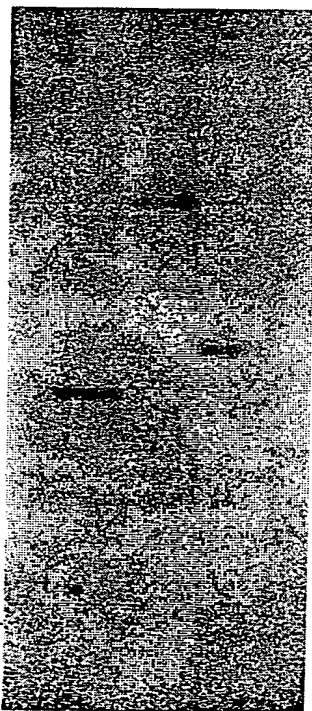


Figure 10

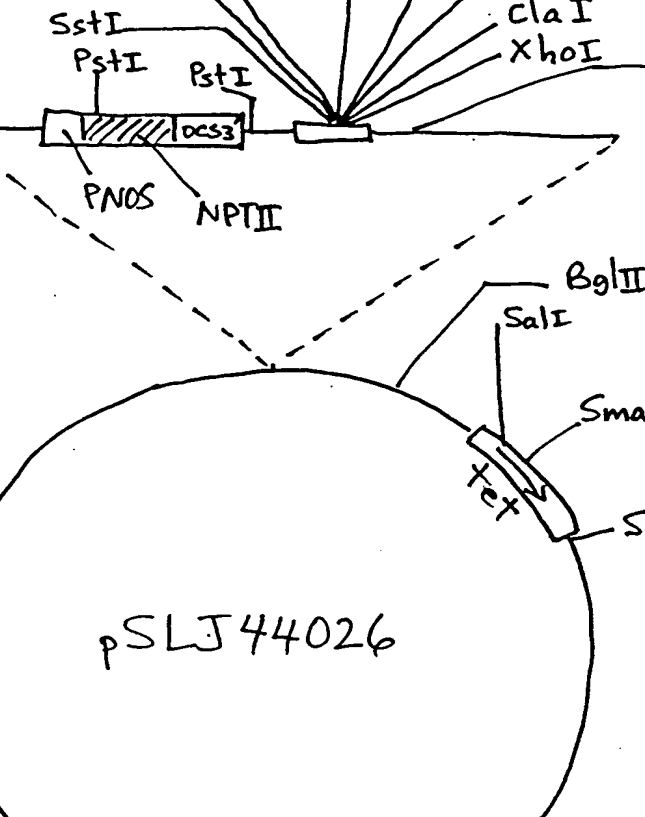


Figure 11